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RAW SEQUENCE LISTING

DATE: 05/02/2002

PATENT APPLICATION: US/10/037,616

TIME: 15:52:56

Input Set : A:\English Sequence Listing.txt

Output Set: N:\CRF3\05022002\J037616.raw

4 <110> APPLICANT: English, Denis
 5 Kovacs, Richard J.
 6 Rizzo, Maria T.
 7 Sliva, Daniel T.
 10 <120> TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
 13 <130> FILE REFERENCE: 7042-119
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/037,616
 C--> 18 <141> CURRENT FILING DATE: 2002-04-19
 21 <150> PRIOR APPLICATION NUMBER: US 60/243,887
 23 <151> PRIOR FILING DATE: 2000-10-27
 26 <160> NUMBER OF SEQ ID NOS: 27
 29 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2776
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (244)..(1386)
 41 <223> OTHER INFORMATION:
 44 <400> SEQUENCE: 1
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 50 cacaaaaagc ctggatcaact catcgaacca cccctgaagc cagtgaaggc tctctcgcc 180
 52 cgccctctag cgttcgtctg gactagcgcc accccggctt cctggggaca cagggttggc 240
 54 acc atg ggg ccc acc agc gtc ccg ctg gtc aag gcc cac cgc agc tcg 288
 55 Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser
 56 1 5 10 15
 58 gtc tct gac tac gtc aac tat gat atc atc gtc cgg cat tac aac tac 336
 59 Val Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr
 60 20 25 30
 62 acg gga aag ctg aat atc agc gcg gac aag gag aac agc att aaa ctg 384
 63 Thr Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu
 64 35 40 45
 66 acc tcg gtg gtg ttc att ctc atc tgc tgc ttt atc atc ctg gag aac 432
 67 Thr Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn
 68 50 55 60
 70 atc ttt gtc ttg ctg acc att tgg aaa acc aag aaa ttc cac cga ccc 480
 71 Ile Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro
 72 65 70 75
 74 atg tac tat ttt att ggc aat ctg gcc ctc tca gac ctg ttg gca gga 528
 75 Met Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly
 76 80 85 90 95

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78	gta gcc tac aca gct aac ctg ctc ttg tct ggg gcc acc acc tac aag	576
79	Val Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys	
80	100 105 110	
82	ctc act ccc gcc cag tgg ttt ctg cgg gaa ggg agt atg ttt gtg gcc	624
83	Leu Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala	
84	115 120 125	
86	ctg tca gcc tcc gtg ttc agt ctc ctc gcc atc gcc att gag cgc tat	672
87	Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr	
88	130 135 140	
90	atc aca atg ctg aaa atg aaa ctc cac aac ggg agc aat aac ttc cgc	720
91	Ile Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg	
92	145 150 155	
94	ctc ttc ctg cta atc agc gcc tgc tgg gtc atc tcc ctc atc ctg ggt	768
95	Leu Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly	
96	160 165 170 175	
98	ggc ctg cct atc atg ggc tgg aac tgc atc agt gcg ctg tcc agc tgc	816
99	Gly Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys	
100	180 185 190	
102	tcc acc gtg ctg ccg ctc tac cac aag cac tat atc ctc ttc tgc acc	864
103	Ser Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr	
104	195 200 205	
106	acg gtc ttc act ctg ctt ctg ctc tcc atc gtc att ctg tac tgc aga	912
107	Thr Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg	
108	210 215 220	
110	atc tac tcc ttg gtc agg act cgg agc cgc cgc ctg acg ttc cgc aag	960
111	Ile Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys	
112	225 230 235	
114	aac att tcc aag gcc agc cgc agc tct gag aag tcg ctg gcg ctg ctc	1008
115	Asn Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu	
116	240 245 250 255	
118	aag acc gta att atc gtc ctg agc gtc ttc atc gcc tgc tgg gca ccg	1056
119	Lys Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro	
120	260 265 270	
122	ctc ttc atc ctg ctc ctg ctg gat gtg ggc tgc aag gtg aag acc tgt	1104
123	Leu Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys	
124	275 280 285	
126	gac atc ctc ttc aga gcg gag tac ttc ctg gtg tta gct gtg ctc aac	1152
127	Asp Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn	
128	290 295 300	
130	tcc ggc acc aac ccc atc att tac act ctg acc aac aag gag atg cgt	1200
131	Ser Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg	
132	305 310 315	
134	cgg gcc ttc atc cgg atc atg tcc tgc tgc aag tgc ccg agc gga gac	1248
135	Arg Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp	
136	320 325 330 335	
138	tct gct ggc aaa ttc aag cga ccc atc atc gcc ggc atg gaa ttc agc	1296
139	Ser Ala Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser	
140	340 345 350	
142	cgc agc aaa tcg gac aat tcc tcc cac ccc cag aaa gac gaa ggg gac	1344

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143 Arg Ser Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp
144          355          360          365
146 aac cca gag acc att atg tct tct gga aac gtc aac tct tct      1386
147 Asn Pro Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser
148          370          375          380
150 tcctagaact ggaagctgtc caccacccgg aagcgcctctt tacttggtcg ctggccaccc      1446
152 cagtgtttgg aaaaaaatct ctgggcttcg actgctgcca gggaggagct gctgcaagcc      1506
154 agagggagga agggggagaa tacgaacagc ctgggtggtg cggtgtgttg tgggtagagt      1566
156 tagttcctgt gaacaatgca ctgggaaggg tggagatcag gtcccggcct ggaatatatt      1626
158 ttctaccccc ctggagcttt gattttgcac tgagccaaag gtctagcatt gtcaagctcc      1686
160 taaagggttc atttggcccc tcctcaaaga ctaatgtccc catgtgaaag cgtctctttg      1746
162 tctggagctt tgaggagatg ttttccttca ctttagtttc aaaccaagt gagtgtgtgc      1806
164 acttctgctt ctttagggat gccctgtaca tcccacaccc caccctccct tcccttcata      1866
166 cccctcctca acgttctttt actttatact ttaactacct gagagtatc agagctgggg      1926
168 ttgtggaatg atcgatcatc tatagcaaat aggctatgtt gagtacgtag gctgtgggaa      1986
170 gatgaagatg gtttggaggt gtaaaacaat gtccttcgct gaggccaaag tttccatgta      2046
172 agcgggatcc gtttttttga atttgggtga agtcaacttg atttctttaa aaaacatctt      2106
174 ttcaatgaaa tgtgttacca tttcatatcc attgaagccg aaatctgcat aaggaagccc      2166
176 actttatcta aatgatatta gccaggatcc ttggtgtcct aggagaaaca gacaagcaaa      2226
178 acaaagttaa aaccgaatgg attaaccttt gcaaaccaag ggagatttct tagcaaatga      2286
180 gtctaacaaa tatgacatct gtctttggca cttttgttga tgtttatttc agaattgtgt      2346
182 gtgattcatt tcaagcaaca acatggttgt attttgttgt gttaaaagta cttttcttga      2406
184 tttttgaatg tatttgtttc agcagaagtc attttatttg atttttctaa cccgtgttaa      2466
186 caccattgaa tgtgtatttc ttaagaaaat accaccctct tgtgccctta aaagcattac      2526
188 tttaactggt agggaacgcc agaaactttt cagtccagct attcattaga tagtaattga      2586
190 agatatgtat aaatattaca aagaataaaa atatattact gtctctttag tatggttttc      2646
192 agtgcaatta aaccgagaga tgtcttgttt ttttaaaaag aatagtattt aataggtttc      2706
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217 cgttcttgcg agccggcctg caggagcgca ggctcccctg gcctcccgca cccagcggcg      180
219 gaccgagccc ctggagggaa gttgccgcag ccgcccgggc cgccggccct cctgtcccgc      240
221 gccaggtaca cagcttctcc tagcatgact tcgatctgat cagcaaacaa gaaaatttgt      300
223 ctcccgtagt tctggggcgt gttcaccacc tacaaccaca gagctgtc atg gct gcc      357
224          Met Ala Ala
225          1
227 atc tct act tcc atc cct gta att tca cag ccc cag ttc aca gcc atg      405
228 Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe Thr Ala Met
229          5          10          15

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231	aat gaa cca cag tgc ttc tac aac gag tcc att gcc ttc ttt tat aac	453
232	Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe Phe Tyr Asn	
233	20 25 30 35	
235	cga agt gga aag cat ctt gcc aca gaa tgg aac aca gtc agc aag ctg	501
236	Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val Ser Lys Leu	
237	40 45 50	
239	gtg atg gga ctt gga atc act gtt tgt atc ttc atc atg ttg gcc aac	549
240	Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met Leu Ala Asn	
241	55 60 65	
243	cta ttg gtc atg gtg gca atc tat gtc aac cgc cgc ttc cat ttt cct	597
244	Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe His Phe Pro	
245	70 75 80	
247	att tat tac cta atg gct aat ctg gct gct gca gac ttc ttt gct ggg	645
248	Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly	
249	85 90 95	
251	ttg gcc tac ttc tat ctc atg ttc aac aca gga ccc aat act cgg aga	693
252	Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn Thr Arg Arg	
253	100 105 110 115	
255	ctg act gtt agc aca tgg ctc ctt cgt cag ggc ctc att gac acc agc	741
256	Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile Asp Thr Ser	
257	120 125 130	
259	ctg acg gca tct gtg gcc aac tta ctg gct att gca atc gag agg cac	789
260	Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile Glu Arg His	
261	135 140 145	
263	att acg gtt ttc cgc atg cag ctc cac aca cgg atg agc aac cgg cgg	837
264	Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser Asn Arg Arg	
265	150 155 160	
267	gta gtg gtg gtc att gtg gtc atc tgg act atg gcc atc gtt atg ggt	885
268	Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile Val Met Gly	
269	165 170 175	
271	gct ata ccc agt gtg ggc tgg aac tgt atc tgt gat att gaa aat tgt	933
272	Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile Glu Asn Cys	
273	180 185 190 195	
275	tcc aac atg gca ccc ctc tac agt gac tct tac tta gtc ttc tgg gcc	981
276	Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val Phe Trp Ala	
277	200 205 210	
279	att ttc aac ttg gtg acc ttt gtg gta atg gtg gtt ctc tat gct cac	1029
280	Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu Tyr Ala His	
281	215 220 225	
283	atc ttt ggc tat gtt cgc cag agg act atg aga atg tct cgg cat agt	1077
284	Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser Arg His Ser	
285	230 235 240	
287	tct gga ccc cgg cgg aat cgg gat acc atg atg agt ctt ctg aag act	1125
288	Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu Leu Lys Thr	
289	245 250 255	
291	gtg gtc att gtg ctt ggg gcc ttt atc atc tgc tgg act cct gga ttg	1173
292	Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr Pro Gly Leu	
293	260 265 270 275	
295	gtt ttg tta ctt cta gac gtg tgc tgt cca cag tgc gac gtg ctg gcc	1221

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296 Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp Val Leu Ala
297                               280                               285                               290
299 tat gag aaa ttc ttc ctt ctc ctt gct gaa ttc aac tct gcc atg aac      1269
300 Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser Ala Met Asn
301                               295                               300                               305
303 ccc atc att tac tcc tac cgc gac aaa gaa atg agc gcc acc ttt agg      1317
304 Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala Thr Phe Arg
305                               310                               315                               320
307 cag atc ctc tgc tgc cag cgc agt gag aac ccc acc gcc ccc aca gaa      1365
308 Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly Pro Thr Glu
309                               325                               330                               335
311 ggc tca gac cgc tcg gct tcc tcc ctc aac cac acc atc ttg gct gga      1413
312 Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile Leu Ala Gly
313 340                               345                               350                               355
315 gtt cac agc aat gac cac tct gtg gtt tagaacgaa actgagatga      1460
316 Val His Ser Asn Asp His Ser Val Val
317                               360
319 ggaaccagcc gtcctctctt ggaggataaa cagcctcccc ctacccaatt gccagggcaa      1520
321 ggtgggggtgt gagagaggag aaaagtcaac tcatgtactt aaacactaac caatgacagt      1580
323 atttggttctt ggaccccaca agacttgata tatattgaaa attagcttat gtgacaacccc      1640
325 tcatcttgat ccccatccct tctgaaagta ggaagttgga gctcttgcaa tgggaattcaa      1700
327 gaacagactc tggagtgtcc atttagacta cactaactag actttttaaaa gatttttgtgt      1760
329 ggtttggtgc aagtcagaat aaattctggc tagttgaatc cacaacttca tttatataca      1820
331 ggcttccctt ttttattttt aaaggatacg tttcacttaa taaacacggt tatgcctatc      1880
333 agcatgtttg tgatggatga gactatggac tgcttttaaa ctaccataat tccatttttt      1940
335 cccttacata ggaaaactgt aagttggaat tatcttttgt ttagaaagca tgcattgtaat      2000
337 gtatgtatgc agtatgcctt acttaaaaaag attaaaagga tactaatggt aaatcttcta      2060
339 ggaaatagaa cctagacttc aaagccagta tttgtttagg tcatgaagca aacaatgctc      2120
341 taatcacaat attaactggt taattaaaaat gttgtaacaa gtataaaaca gggaatgtaa      2180
343 gtttattacc aaagtgatat gtattccaaa aaagtcatag aagatgaagc actataatat      2240
345 tgttcccata tatttaaaat acccaagtac attctaatta ccagtatatc agaggaaaat      2300
347 tttcgtagtc tttgtaaaaat aatatactca tcatagaaaa cttgaaaaat acagaaatgt      2360
349 ataaaaaagc aaaaatgatt actgataata tcacaaccca gaagtaacca cctttaaaaa      2420
351 gcaaccccca tgtatgccta tatgtgtatt gtatactttt tttacataat tggagtcata      2480
353 ctgtaaacag ttttataagt agatcttttt cattgcaaaa ttgccacatt ttcttatggc      2540
355 attaaaaatt ttacaaaaac ataatttttaa tggctatatt atattccatt taatggatgc      2600
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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date